Natasa Przulj

List of Publications by Year
in descending order

100 papers	7,335 citations	93792 39 h-index	71088 80 g-index
106 all docs	106 docs citations	106 times ranked	10489 citing authors

#	Article	IF	Citations
1	Graphlet eigencentralities capture novel central roles of genes in pathways. PLoS ONE, 2022, 17, e0261676.	1.1	2
2	Classification in biological networks with hypergraphlet kernels. Bioinformatics, 2021, 37, 1000-1007.	1.8	9
3	Integrative Data Analytic Framework to Enhance Cancer Precision Medicine. Network and Systems Medicine, 2021, 4, 60-73.	2.7	2
4	Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. Scientific Reports, 2021, 11, 18985.	1.6	5
5	Antiproliferative activity and mode of action analysis of novel amino and amido substituted phenantrene and naphtho[2,1-b]thiophene derivatives. European Journal of Medicinal Chemistry, 2020, 185, 111833.	2.6	13
6	Unveiling new disease, pathway, and gene associations via multi-scale neural network. PLoS ONE, 2020, 15, e0231059.	1.1	18
7	Probabilistic graphlets capture biological function in probabilistic molecular networks. Bioinformatics, 2020, 36, i804-i812.	1.8	4
8	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
9	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
10	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
11	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
12	Graphlet Laplacians for topology-function and topology-disease relationships. Bioinformatics, 2019, 35, 5226-5234.	1.8	8
13	Introduction to Graph and Network Theory. , 2019, , 111-150.		0
14	Graphlets in Network Science and Computational Biology. , 2019, , 193-240.		2
15	Machine Learning for Data Integration in Cancer Precision Medicine: Matrix Factorization Approaches. , 2019, , 286-312.		0
16	Network Alignment. , 2019, , 369-413.		1
17	Functional geometry of protein interactomes. Bioinformatics, 2019, 35, 3727-3734.	1.8	5
18	Towards a data-integrated cell. Nature Communications, 2019, 10, 805.	5.8	37

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19	Precision medicine â€¢ A promising, yet challenging road lies ahead. Current Opinion in Systems Biology, 2018, 7, 1-7.	1.3	13
20	Critical Review on Zeolite Clinoptilolite Safety and Medical Applications in vivo. Frontiers in Pharmacology, 2018, 9, 1350.	1.6	137
21	Higher-order molecular organization as a source of biological function. Bioinformatics, 2018, 34, i944-i953.	1.8	32
22	Rebuttal to the Letter to the Editor in response to the paper: proper evaluation of alignment-free network comparison methods. Bioinformatics, 2017, 33, 1107-1109.	1.8	1
23	Unified Alignment of Protein-Protein Interaction Networks. Scientific Reports, 2017, 7, 953.	1.6	40
24	Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. Journal of Integrative Bioinformatics, 2017, 14, .	1.0	0
25	Systematic proteinâ€"protein interaction mapping for clinically relevant human <scp>GPCR</scp>s. Molecular Systems Biology, 2017, 13, 918.	3.2	63
26	Network analytics in the age of big data. Science, 2016, 353, 123-124.	6.0	77
27	PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. , 2016, , .		27
28	Graphlet-based Characterization of Directed Networks. Scientific Reports, 2016, 6, 35098.	1.6	68
29	A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, .	6.0	979
30	Computational Methods for Integration of Biological Data. Europeanization and Globalization, 2016, , 137-178.	0.1	2
31	Integrative methods for analyzing big data in precision medicine. Proteomics, 2016, 16, 741-758.	1.3	149
32	Fuse: multiple network alignment via data fusion. Bioinformatics, 2016, 32, 1195-1203.	1.8	42
33	PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 321-32.	0.7	15
34	Methods for biological data integration: perspectives and challenges. Journal of the Royal Society Interface, 2015, 12, 20150571.	1.5	196
35	L-GRAAL: Lagrangian graphlet-based network aligner. Bioinformatics, 2015, 31, 2182-2189.	1.8	112
36	Proper evaluation of alignment-free network comparison methods. Bioinformatics, 2015, 31, 2697-2704.	1.8	46

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37	Topology-function conservation in protein–protein interaction networks. Bioinformatics, 2015, 31, 1632-1639.	1.8	62
38	ergm.graphlets: A Package for ERG Modeling Based on Graphlet Statistics. Journal of Statistical Software, 2015, 65, .	1.8	13
39	Integration of molecular network data reconstructs Gene Ontology. Bioinformatics, 2014, 30, i594-i600.	1.8	30
40	Survey of Network-Based Approaches to Research of Cardiovascular Diseases. BioMed Research International, 2014, 2014, 1-10.	0.9	8
41	Network wiring of pleiotropic kinases yields insight into protective role of diabetes on aneurysm. Integrative Biology (United Kingdom), 2014, 6, 1049-1057.	0.6	6
42	Anti-nicastrin monoclonal antibodies elicit pleiotropic anti-tumour pharmacological effects in invasive breast cancer cells. Breast Cancer Research and Treatment, 2014, 148, 455-462.	1.1	22
43	Predicting disease associations via biological network analysis. BMC Bioinformatics, 2014, 15, 304.	1.2	86
44	The integrated disease network. Integrative Biology (United Kingdom), 2014, 6, 1069-1079.	0.6	28
45	The role of genes co-amplified with nicastrin in breast invasive carcinoma. Breast Cancer Research and Treatment, 2014, 143, 393-401.	1.1	6
46	GR-Align: fast and flexible alignment of protein 3D structures using graphlet degree similarity. Bioinformatics, 2014, 30, 1259-1265.	1.8	55
47	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	1.0	38
48	The Topology of the Growing Human Interactome Data. Journal of Integrative Bioinformatics, 2014, 11, 27-42.	1.0	5
49	Revealing the Hidden Language of Complex Networks. Scientific Reports, 2014, 4, 4547.	1.6	153
50	Modelling the Yeast Interactome. Scientific Reports, 2014, 4, 4273.	1.6	14
51	The topology of the growing human interactome data. Journal of Integrative Bioinformatics, 2014, 11, 238.	1.0	5
52	Discovering disease-disease associations by fusing systems-level molecular data. Scientific Reports, 2013, 3, 3202.	1.6	96
53	Graphlet-based measures are suitable for biological network comparison. Bioinformatics, 2013, 29, 483-491.	1.8	71
54	Network Topology Reveals Key Cardiovascular Disease Genes. PLoS ONE, 2013, 8, e71537.	1.1	44

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55	Biological function through network topology: a survey of the human diseasome. Briefings in Functional Genomics, 2012, 11, 522-532.	1.3	45
56	C-GRAAL: Common-neighbors-based global GRAph ALignment of biological networks. Integrative Biology (United Kingdom), 2012, 4, 734.	0.6	79
57	Protein Complex Prediction with RNSC. Methods in Molecular Biology, 2012, 804, 297-312.	0.4	15
58	The Core Diseasome. Molecular BioSystems, 2012, 8, 2614.	2.9	40
59	Topological Characteristics of Molecular Networks. , 2012, , 15-48.		5
60	A framework for FPGA acceleration of large graph problems: Graphlet counting case study. , 2011, , .		33
61	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	6.0	838
62	Dominating Biological Networks. PLoS ONE, 2011, 6, e23016.	1.1	85
63	GraphCrunch 2: Software tool for network modeling, alignment and clustering. BMC Bioinformatics, 2011, 12, 24.	1.2	63
64	Proteinâ€protein interactions: Making sense of networks via graphâ€theoretic modeling. BioEssays, 2011, 33, 115-123.	1.2	66
65	Introduction to the Special Issue on Biological Networks. Internet Mathematics, 2011, 7, 207-208.	0.7	2
66	Integrative network alignment reveals large regions of global network similarity in yeast and human. Bioinformatics, 2011, 27, 1390-1396.	1.8	217
67	Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. BMC Systems Biology, 2010, 4, 84.	3.0	32
68	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, 275-289.	1.0	20
69	Optimal Network Alignment with Graphlet Degree Vectors. Cancer Informatics, 2010, 9, CIN.S4744.	0.9	149
70	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	14
71	Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data. Journal of the Royal Society Interface, 2010, 7, 423-437.	1.5	95
72	Biological network comparison using graphlet degree distribution. Bioinformatics, 2010, 26, 853-854.	1.8	21

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73	Topological network alignment uncovers biological function and phylogeny. Journal of the Royal Society Interface, 2010, 7, 1341-1354.	1.5	281
74	Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy. Journal of Proteome Research, 2010, 9, 2016-2029.	1.8	51
75	From Topology to Phenotype in Protein–Protein Interaction Networks. , 2010, , 31-49.		1
76	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	8
77	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	17
78	Optimized Null Model for Protein Structure Networks. PLoS ONE, 2009, 4, e5967.	1.1	34
79	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
80	Geometric De-noising of Protein-Protein Interaction Networks. PLoS Computational Biology, 2009, 5, e1000454.	1.5	158
81	Structure of brain functional networks. , 2009, 2009, 4166-70.		5
82	GEOMETRIC EVOLUTIONARY DYNAMICS OF PROTEIN INTERACTION NETWORKS. , 2009, , 178-189.		29
83	Learning the structure of protein-protein interaction networks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 39-50.	0.7	6
84	GraphCrunch: A tool for large network analyses. BMC Bioinformatics, 2008, 9, 70.	1.2	93
85	Fitting a geometric graph to a protein–protein interaction network. Bioinformatics, 2008, 24, 1093-1099.	1.8	109
86	Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein interaction network analysis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13333-13338.	3.3	129
87	LEARNING THE STRUCTURE OF PROTEIN-PROTEIN INTERACTION NETWORKS. , 2008, , .		8
88	Uncovering Biological Network Function via Graphlet Degree Signatures. Cancer Informatics, 2008, 6, CIN.S680.	0.9	200
89	Uncovering biological network function via graphlet degree signatures. Cancer Informatics, 2008, 6, 257-73.	0.9	96
90	Not All Scale-Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Evolution. PLoS Computational Biology, 2007, 3, e118.	1.5	77

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91	Biological network comparison using graphlet degree distribution. Bioinformatics, 2007, 23, e177-e183.	1.8	612
92	Geometric Local Structure in Biological Networks. , 2007, , .		2
93	Modelling protein–protein interaction networks via a stickiness index. Journal of the Royal Society Interface, 2006, 3, 711-716.	1.5	76
94	Not All Scale Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Emulation. Lecture Notes in Computer Science, 2006, , 1-13.	1.0	0
95	2-Tree probe interval graphs have a large obstruction set. Discrete Applied Mathematics, 2005, 150, 216-231.	0.5	10
96	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. Science, 2005, 307, 1621-1625.	6.0	651
97	Hereditary dominating pair graphs. Discrete Applied Mathematics, 2004, 134, 239-261.	0.5	4
98	Minimum Average Time Broadcast Graphs. Parallel Processing Letters, 1998, 08, 139-147.	0.4	0
99	Biological networks uncover evolution, disease, and gene functions. , 0, , 291-314.		0
100	Four algorithms to solve symmetric multi-type non-negative matrix tri-factorization problem. Journal of Global Optimization, 0, , 1.	1.1	1